

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 23:02:39 ; Search time 356.058 Seconds  
(without alignments)  
384.253 Million cell updates/sec

Title: US-10-089-177-697

Perfect score: 23

Sequence: 1 cnaacnfrckncrcrcrcrcg 23

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum March 0\*

Maximum March 100\*

Listing first 500 summaries

Database :

Published Applications NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*

12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*

13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*

14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*

15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*

16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*

17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*

18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*

19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*

20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*

21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	17.4	75.7	23	US-09-989-643-108 Sequence 108, App
2	17.4	75.7	23	US-10-753-169-108 Sequence 108, App
3	17.4	75.7	24	US-10-391-249-35 Sequence 35, App
4	17.4	75.7	98	US-09-815-242-607 Sequence 607, App
5	17.4	75.7	98	US-10-282-122A-626 Sequence 626, App
6	17.4	75.7	108	US-10-282-122A-2940 Sequence 2940, App
7	17.4	75.7	108	US-10-282-122A-3089 Sequence 3089, App
8	17.4	75.7	108	US-10-282-122A-3372 Sequence 3372, App
9	17.4	75.7	122	US-10-282-122A-1095 Sequence 1095, App
c 10	17.4	75.7	186	US-10-282-122A-11867 Sequence 11867, A
11	17.4	75.7	298	US-09-815-242-608 Sequence 608, App

12	17.4	75.7	298	US-10-282-122A-633 Sequence 633, App
13	17.4	75.7	305	US-09-815-242-2764 Sequence 2764, App
14	17.4	75.7	305	US-10-282-122A-2664 Sequence 2664, App
15	17.4	75.7	305	US-10-282-122A-5304 Sequence 5304, App
16	17.4	75.7	341	US-10-282-122A-2431 Sequence 2431, App
17	17.4	75.7	383	US-10-282-122A-2253 Sequence 2253, App
18	17.4	75.7	402	US-10-282-122A-8376 Sequence 8376, App
c 19	17.4	75.7	402	US-10-282-122A-19466 Sequence 19466, A
20	17.4	75.7	447	US-10-282-122A-2476 Sequence 2476, App
c 21	17.4	75.7	448	US-10-282-122A-12826 Sequence 12826, A
c 22	17.4	75.7	468	US-10-282-122A-37380 Sequence 37380, A
c 23	17.4	75.7	882	US-09-989-643-149 Sequence 149, App
c 24	17.4	75.7	882	US-10-391-249-21 Sequence 21, App
c 25	17.4	75.7	882	US-10-753-169-149 Sequence 149, App
c 26	17.4	75.7	885	US-09-989-643-148 Sequence 148, App
c 27	17.4	75.7	885	US-10-753-169-148 Sequence 148, App
c 28	17.4	75.7	887	US-10-391-249-20 Sequence 20, App
c 29	17.4	75.7	888	US-09-989-643-152 Sequence 152, App
c 30	17.4	75.7	888	US-10-753-169-152 Sequence 152, App
c 31	17.4	75.7	891	US-09-989-643-154 Sequence 154, App
c 32	17.4	75.7	891	US-09-989-643-155 Sequence 155, App
c 33	17.4	75.7	891	US-09-989-643-157 Sequence 157, App
c 34	17.4	75.7	891	US-09-989-643-159 Sequence 159, App
c 35	17.4	75.7	891	US-09-989-643-160 Sequence 160, App
c 36	17.4	75.7	891	US-09-989-643-160 Sequence 160, App
c 37	17.4	75.7	891	US-09-989-643-162 Sequence 162, App
c 38	17.4	75.7	891	US-09-989-643-163 Sequence 163, App
c 39	17.4	75.7	891	US-09-989-643-164 Sequence 164, App
c 40	17.4	75.7	891	US-10-753-169-154 Sequence 154, App
c 41	17.4	75.7	891	US-10-753-169-155 Sequence 155, App
c 42	17.4	75.7	891	US-10-753-169-157 Sequence 157, App
c 43	17.4	75.7	891	US-10-753-169-159 Sequence 159, App
c 44	17.4	75.7	891	US-10-753-169-160 Sequence 160, App
c 45	17.4	75.7	891	US-10-753-169-161 Sequence 161, App
c 46	17.4	75.7	891	US-10-753-169-162 Sequence 162, App
c 47	17.4	75.7	891	US-10-753-169-163 Sequence 163, App
c 48	17.4	75.7	891	US-10-753-169-164 Sequence 164, App
c 49	17.4	75.7	894	US-09-989-643-151 Sequence 151, App
c 50	17.4	75.7	894	US-09-989-643-156 Sequence 156, App
c 51	17.4	75.7	894	US-09-989-643-167 Sequence 167, App
c 52	17.4	75.7	894	US-10-753-169-151 Sequence 151, App
c 53	17.4	75.7	894	US-10-753-169-156 Sequence 156, App
c 54	17.4	75.7	894	US-10-753-169-167 Sequence 167, App
c 55	17.4	75.7	897	US-09-989-643-147 Sequence 147, App
c 56	17.4	75.7	897	US-09-989-643-166 Sequence 166, App
c 57	17.4	75.7	897	US-09-989-643-168 Sequence 168, App
c 58	17.4	75.7	897	US-10-753-169-147 Sequence 147, App
c 59	17.4	75.7	897	US-10-753-169-166 Sequence 166, App
c 60	17.4	75.7	897	US-10-753-169-168 Sequence 168, App
c 61	17.4	75.7	906	US-09-989-643-158 Sequence 158, App
c 62	17.4	75.7	906	US-10-753-169-158 Sequence 158, App
c 63	17.4	75.7	909	US-09-989-643-171 Sequence 171, App
c 64	17.4	75.7	909	US-10-753-169-171 Sequence 171, App
c 65	17.4	75.7	918	US-10-282-122A-31617 Sequence 31617, A
c 66	17.4	75.7	950	US-10-282-122A-23136 Sequence 23136, A
c 67	17.4	75.7	1170	US-10-156-761-7006 Sequence 7006, App
c 68	17.4	75.7	1182	US-09-815-242-4519 Sequence 4519, App
c 69	17.4	75.7	1182	US-10-282-122A-12755 Sequence 12755, A
c 70	17.4	75.7	1182	US-10-282-122A-19744 Sequence 19744, A
c 71	17.4	75.7	1182	US-10-282-122A-23175 Sequence 23175, A
c 72	17.4	75.7	1182	US-10-282-122A-29230 Sequence 29230, A
c 73	17.4	75.7	1182	US-10-282-122A-32228 Sequence 32228, A
c 74	17.4	75.7	1182	US-10-282-122A-34285 Sequence 34285, A
c 75	17.4	75.7	1182	US-10-282-122A-35489 Sequence 35489, A
c 76	17.4	75.7	1182	US-10-282-122A-35489 Sequence 35489, A
c 77	17.4	75.7	1182	US-10-470-0488-115 Sequence 115, App
c 78	17.4	75.7	1182	US-10-282-122A-37061 Sequence 37061, A
c 79	17.4	75.7	1185	US-09-912-020-86 Sequence 86, App
c 80	17.4	75.7	1185	US-09-815-242-3832 Sequence 3832, App
c 81	17.4	75.7	1185	US-09-815-242-6265 Sequence 6265, App
c 82	17.4	75.7	1185	US-09-815-242-6334 Sequence 6334, App
c 83	17.4	75.7	1185	US-09-815-242-6962 Sequence 6962, App
c 84	17.4	75.7	1185	US-09-815-242-6972 Sequence 6972, App

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OM nucleic - nucleic search, using sw model

Run on: March 16, 2005, 01:07:34 ; Search time 87.1346 Seconds  
(without alignments)  
431.911 Million cell updates/sec

Title: US-10-089-177-697

Perfect score: 23

Sequence: 1 ccmangtncncrcrcrcrcg 23

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameterb: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents NA.\*

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4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*

5: /cgn2\_6/ptodata/1/ina/6C.COMB.seq.\*

6: /cgn2\_6/ptodata/1/ina/6D.COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	75.7	189	4	US-09-107-532A-3602
2	17.4	75.7	297	4	US-09-252-991A-4695
3	17.4	75.7	330	4	US-09-107-532A-1603
4	17.4	75.7	498	4	US-09-902-540-7475
5	17.4	75.7	609	4	US-09-107-433-2243
6	17.4	75.7	785	4	US-09-154-083-229
7	17.4	75.7	1122	4	US-09-134-000C-1261
8	17.4	75.7	1131	4	US-09-107-532A-979
9	17.4	75.7	1155	4	US-09-328-352-1547
10	17.4	75.7	1185	2	US-08-743-637B-185
11	17.4	75.7	1185	4	US-09-218-197-1
12	17.4	75.7	1185	4	US-09-492-708A-86
13	17.4	75.7	1191	4	US-09-107-532A-1379
14	17.4	75.7	1191	4	US-09-902-540-8380
15	17.4	75.7	1197	4	US-09-583-110-747
16	17.4	75.7	1224	4	US-09-452-991A-4775
17	17.4	75.7	1230	4	US-09-252-991A-4733
18	17.4	75.7	1230	4	US-09-252-991A-4767
19	17.4	75.7	1245	3	US-09-134-001C-2540
20	17.4	75.7	1254	4	US-09-489-039A-3750
21	17.4	75.7	1260	4	US-09-489-039A-3750
22	17.4	75.7	1356	4	US-09-252-991A-4740
23	17.4	75.7	2996	3	US-08-961-527-260
24	17.4	75.7	3719	1	US-08-920-812-10
25	17.4	75.7	3719	1	US-08-920-827-10
26	17.4	75.7	3719	1	US-08-921-177-10
27	17.4	75.7	3719	1	US-08-362-577C-10

28	17.4	75.7	3719	2	US-08-920-828-10	Sequence 10, Appl
29	17.4	75.7	5787	4	US-09-902-540-722	Sequence 722, App
30	17.4	75.7	7035	4	US-09-902-540-878	Sequence 878, App
31	17.4	75.7	15598	4	US-08-956-171E-82	Sequence 82, Appl
32	17.4	75.7	15598	4	US-08-781-986A-82	Sequence 82, Appl
33	17.4	75.7	49617	4	US-09-596-002-28	Sequence 28, Appl
34	17.4	75.7	580073	4	US-08-545-528D-1	Sequence 1, Appl
35	17.4	75.7	640681	4	US-09-790-988-1	Sequence 1, Appl
36	17.4	75.7	1830121	4	US-09-557-884-1	Sequence 1, Appl
37	17.4	75.7	1830121	4	US-09-557-884-1	Sequence 1, Appl
38	17.4	75.7	1830121	4	US-09-643-990A-1	Sequence 1, Appl
39	17.4	75.7	1830121	4	US-09-643-990A-1	Sequence 1, Appl
40	17.4	75.7	4403765	3	US-09-103-840A-2	Sequence 2, Appl
41	17.4	75.7	4411529	3	US-09-103-840A-1	Sequence 1, Appl
42	15.8	68.7	489	4	US-09-252-991A-10298	Sequence 10298, A
43	15.8	68.7	601	4	US-09-949-016-204917	Sequence 204917, A
44	15.8	68.7	601	4	US-09-949-016-204917	Sequence 204918, A
45	15.8	68.7	651	4	US-09-902-540-4369	Sequence 4369, App
46	15.8	68.7	1689	4	US-09-902-540-3347	Sequence 3347, App
47	15.8	68.7	3231	1	US-08-074-121-4	Sequence 4, Appl
48	15.8	68.7	3231	5	PCT-US94-06447-4	Sequence 4, Appl
49	15.8	68.7	9790	4	US-09-949-016-17204	Sequence 17204, A
50	15.8	68.7	11935	4	US-09-634-238-401	Sequence 401, App
51	15.8	68.7	12001	1	US-08-458-568A-11	Sequence 11, Appl
52	15.8	68.7	15287	4	US-09-949-016-17203	Sequence 17203, A
53	15.8	68.7	15337	4	US-09-902-540-1157	Sequence 1157, App
54	15.8	68.7	23694	4	US-09-902-540-1216	Sequence 1216, App
55	15.8	68.7	31063	4	US-09-596-002-20	Sequence 20, Appl
56	15.8	68.7	39376	4	US-09-949-016-17536	Sequence 17536, A
57	15.8	68.7	1230025	4	US-09-198-452A-1	Sequence 1, Appl
58	15.8	68.7	1230230	3	US-09-438-185A-1	Sequence 1, Appl
59	15.8	68.7	4403765	3	US-09-103-840A-1	Sequence 2, Appl
60	15.8	68.7	4411529	3	US-09-103-840A-1	Sequence 1, Appl
61	15.2	66.1	5198	1	US-08-123-761A-1	Sequence 13, Appl
62	14.8	64.3	30	1	US-08-207-901-13	Sequence 2404, App
63	14.8	64.3	341	4	US-09-621-976-2404	Sequence 169225, A
64	14.8	64.3	601	4	US-09-949-016-169225	Sequence 166119, A
65	14.8	64.3	601	4	US-09-949-016-186119	Sequence 6042, App
66	14.8	64.3	867	4	US-09-902-540-6042	Sequence 2404, App
67	14.8	64.3	243	4	US-09-902-540-243	Sequence 19747, A
68	14.8	64.3	933	4	US-09-902-540-9341	Sequence 9341, App
69	14.8	64.3	1044	3	US-09-921-017B-113	Sequence 113, App
70	14.8	64.3	1430	4	US-09-976-354-878	Sequence 878, App
71	14.8	64.3	1509	4	US-09-602-777A-211	Sequence 211, App
72	14.8	64.3	2007	4	US-09-902-540-8607	Sequence 8607, App
73	14.8	64.3	2286	4	US-09-800-729-43	Sequence 43, Appl
74	14.8	64.3	2329	4	US-09-800-729-11	Sequence 11, Appl
75	14.8	64.3	2355	4	US-09-902-540-909	Sequence 909, App
76	14.8	64.3	6961	4	US-09-949-016-4770	Sequence 4770, App
77	14.8	64.3	7552	4	US-09-902-540-7552	Sequence 19747, App
78	14.8	64.3	14864	4	US-09-949-016-17047	Sequence 17047, A
79	14.8	64.3	14516	4	US-09-949-016-14516	Sequence 14516, A
80	14.8	64.3	45314	4	US-09-949-016-14927	Sequence 14927, A
81	14.8	64.3	5218	4	US-09-335-409-1	Sequence 1, Appl
82	14.8	64.3	65750	3	US-09-568-480-1	Sequence 1, Appl
83	14.8	64.3	65750	3	US-09-568-480-1	Sequence 1, Appl
84	14.8	64.3	65750	3	US-09-568-480-1	Sequence 1, Appl
85	14.8	64.3	65750	3	US-09-568-480-1	Sequence 1, Appl
86	14.8	64.3	65750	3	US-09-568-480-1	Sequence 1, Appl
87	14.8	64.3	65750	3	US-09-568-480-1	Sequence 1, Appl
88	14.8	64.3	65750	3	US-09-568-480-1	Sequence 1, Appl
89	14.8	64.3	65750	3	US-09-568-480-1	Sequence 1, Appl
90	14.8	64.3	100836	4	US-09-949-016-12871	Sequence 12871, A
91	14.8	64.3	100837	4	US-09-949-016-17063	Sequence 17063, A
92	14.6	63.5	574	3	US-09-073-297-23	Sequence 23, Appl
93	14.6	63.5	574	4	US-09-949-016-91810	Sequence 91810, A
94	14.6	63.5	601	4	US-09-949-016-194751	Sequence 194751, A
95	14.6	63.5	1299	4	US-09-902-540-4780	Sequence 4780, App
96	14.6	63.5	1299	4	US-09-902-540-4780	Sequence 1166, App
97	14.6	63.5	27903	4	US-09-902-540-1235	Sequence 1235, App
98	14.6	63.5	197336	4	US-09-949-016-12881	Sequence 12881, A
99	14.6	63.5	197337	4	US-09-949-016-14376	Sequence 14376, A
100	14.6	63.5	234286	4	US-09-949-016-17272	Sequence 17272, A

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 22:27:13 ; Search time 2312.38 Seconds  
(without alignments)  
378.604 Million cell updates/sec

Title: US-10-089-177-697

Perfect score: 23  
Sequence: 1 cnaacnctknccrcycrcg 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 500 summaries

Database :  
EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic1:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsa1:\*  
9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17.4	75.7	190	6	CD163898 MLI-0084T
2	17.4	75.7	259	6	CD180022 MSI-0021T
3	17.4	75.7	365	7	CN028509 UMC-Pb11v
4	17.4	75.7	372	7	CN026743 UMC-Pd41v
5	17.4	75.7	422	1	AU007630 AU007630
6	17.4	75.7	465	1	AU010926 AU010926
7	17.4	75.7	518	5	BQ811177 1030021B0
8	17.4	75.7	527	5	BQ821806 1030095C0
9	17.4	75.7	539	5	BQ812860 1030032H0
10	17.4	75.7	566	5	BQ815804 1030053A0
11	17.4	75.7	570	8	CC107141 NDL.13F13
12	17.4	75.7	579	5	BQ809961 1030014D0
13	17.4	75.7	626	5	BQ809962 1030014D0
14	17.4	75.7	637	5	BQ811176 1030021B0
15	17.4	75.7	712	7	CO755154 MdlrC3048
16	17.4	75.7	718	7	CO255523 W800825.B
17	17.4	75.7	777	9	CL695862 PRI017C.B
18	17.4	75.7	1122	8	BZ549591 Pac81-60
19	16.4	71.3	424	6	CB302190 TGEStzyE5
20	16.4	71.3	471	6	CB302236 TGEStzyE5
21	16.4	71.3	505	2	BF252980 EST445475
22	16.4	71.3	531	7	CO151838 EST826891
23	16.4	71.3	538	6	CA153033 SCJPR2203
24	16.4	71.3	545	7	CF939964 NCESTgabs

25	16.4	71.3	556	7	CF883816 tric035xo
26	16.4	71.3	582	5	BP176275 BP176275
27	16.4	71.3	589	7	CO134814 EST829485
28	16.4	71.3	592	7	CO145295 EST820348
29	16.4	71.3	614	7	CO151287 EST826340
30	16.4	71.3	637	7	CF387912 RTDR1_17
31	16.4	71.3	646	7	CV516454 0048P0015
32	16.4	71.3	748	7	CO005587 EST793922
33	16.4	71.3	759	7	CF816095 EST693477
34	16.4	71.3	784	7	CO005588 EST793923
35	16.4	71.3	801	8	BZ54176 OGAOT931M
36	16.4	71.3	844	7	CO013017 EST801352
37	16.4	71.3	862	7	CO006264 EST794599
38	16.4	71.3	864	7	CO035000 EST813384
39	16.4	71.3	874	2	BP210517 601874743
40	16.4	71.3	885	7	CO005704 EST794039
41	16.4	71.3	912	7	CF822001 EST699383
42	16.4	71.3	917	7	CO024761 EST803145
43	16.4	71.3	943	7	CO005703 EST794038
44	16.4	71.3	965	7	CO013018 EST801353
45	16.4	71.3	993	7	CO011949 EST800284
46	16.4	71.3	997	7	CO012398 EST800733
47	16.4	71.3	1021	7	CO013654 EST801989
48	16.4	71.3	1035	7	CO009743 EST798078
49	16.4	71.3	1052	7	CO009560 EST797895
50	16.2	70.4	372	2	BE012230 945015F07
51	16.2	70.4	453	5	BK548810 BK548810
52	16.2	70.4	521	7	CO373708 MUR019D02
53	16.2	70.4	527	1	AU294800 AU294800
54	16.2	70.4	527	5	BUS82391 946188H06
55	16.2	70.4	537	6	CB603919 3529.1.53
56	16.2	70.4	545	2	AM065606 614056B07
57	16.2	70.4	581	7	CO513116 3530.1.20
58	16.2	70.4	593	6	CA293879 SCSEGV100
59	16.2	70.4	598	5	BQ295679 1091041B1
60	16.2	70.4	601	6	CA157547 SCEZR2301
61	16.2	70.4	602	6	CA144349 SCRRRT201
62	16.2	70.4	605	6	CA828642 1114031C0
63	16.2	70.4	606	1	AU295857 AU295857
64	16.2	70.4	609	2	AM037181 614021B08
65	16.2	70.4	609	6	CD428143 ETH1_32.F
66	16.2	70.4	620	6	CA190991 SCCRT2C0
67	16.2	70.4	622	5	CA078183 SCRFAM102
68	16.2	70.4	631	5	BQ487172 1091051P1
69	16.2	70.4	659	6	CA213034 SCBSST310
70	16.2	70.4	668	7	CA153871 SCVPR2203
71	16.2	70.4	668	7	CK863732 35011.In
72	16.2	70.4	671	7	CV472864 21014.1.D
73	16.2	70.4	676	6	CB669932 OSJNE02M
74	16.2	70.4	704	7	CK765620 aam01-5ms
75	16.2	70.4	710	4	BG464592 EMI_71.F1
76	16.2	70.4	722	5	BQ087411 Cr1_10.D0
77	16.2	70.4	730	7	CN203557 TOR1852.G
78	16.2	70.4	737	7	CN149202 WOUND1_61
79	16.2	70.4	738	7	CN149691 WOUND1_64
80	16.2	70.4	741	6	CB635325 OS1EB15C
81	16.2	70.4	746	6	BG319815 Zm03_0810
82	16.2	70.4	813	6	CB634299 OS1EB13L
83	16.2	70.4	814	7	CN145785 WOUND1_35
84	16.2	70.4	827	6	CA276170 SCCGSD109
85	16.2	70.4	835	9	CG183637 PUFZK36TD
86	16.2	70.4	936	9	CG101716 PUFKX95TB
87	16.2	70.4	1192	5	BQ212311 AGENCOURT
88	16.2	70.4	1255	3	AY108591 Zea_mays
89	16.2	70.4	1666	2	BG025600 602274526
90	15.8	68.7	138	2	BE518692 946074C08
91	15.8	68.7	222	4	BJS46812 BJS46812
92	15.8	68.7	224	4	BJS46790 BJS46790
93	15.8	68.7	249	1	AV943089 AV943089
94	15.8	68.7	259	1	AV084980 AV084980
95	15.8	68.7	264	6	CA681688 wlm24.DK0
96	15.8	68.7	268	1	AU248181 AU248181
97	15.8	68.7	272	6	CA282200 SCAGSD204

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:46:58 ; Search time 296.346 Seconds  
(without alignments)  
459.443 Million cell updates/sec

Title: US-10-089-177-697

Perfect score: 23

Sequence: 1 cnaacnfnckncrcrcycrcg 23

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : N\_Geneseq\_16Dec04:\*

- 1: geneseqn19808:\*
- 2: geneseqn19908:\*
- 3: geneseqn20008:\*
- 4: geneseqn20018:\*
- 5: geneseqn20028:\*
- 6: geneseqn20038:\*
- 7: geneseqn20048:\*
- 8: geneseqn20058:\*
- 9: geneseqn20068:\*
- 10: geneseqn20078:\*
- 11: geneseqn20088:\*
- 12: geneseqn20098:\*
- 13: geneseqn20108:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	75.7	23	AAV37107	AAV37107 Oligonuc
2	17.4	75.7	23	AAH00706	AAH00706 Universal
3	17.4	75.7	24	AAH00706	AAH00706 M. hyo
4	17.4	75.7	98	AAH00706	AAH00706 M. hyo
5	17.4	75.7	98	AAH00706	AAH00706 M. hyo
6	17.4	75.7	108	AAH00706	AAH00706 M. hyo
7	17.4	75.7	108	AAH00706	AAH00706 M. hyo
8	17.4	75.7	108	AAH00706	AAH00706 M. hyo
9	17.4	75.7	122	AAH00706	AAH00706 M. hyo
10	17.4	75.7	135	AAH00706	AAH00706 M. hyo
11	17.4	75.7	186	AAH00706	AAH00706 M. hyo
12	17.4	75.7	189	AAH00706	AAH00706 M. hyo
13	17.4	75.7	297	AAH00706	AAH00706 M. hyo
14	17.4	75.7	298	AAH00706	AAH00706 M. hyo
15	17.4	75.7	298	AAH00706	AAH00706 M. hyo
16	17.4	75.7	305	AAH00706	AAH00706 M. hyo
17	17.4	75.7	305	AAH00706	AAH00706 M. hyo
18	17.4	75.7	305	AAH00706	AAH00706 M. hyo
19	17.4	75.7	330	AAH00706	AAH00706 M. hyo
20	17.4	75.7	341	AAH00706	AAH00706 M. hyo

21	17.4	75.7	383	8	ACA14383	ACA14383 Prokaryot
22	17.4	75.7	402	8	ACA20506	ACA20506 Prokaryot
23	17.4	75.7	402	8	ACA31596	ACA31596 Prokaryot
24	17.4	75.7	402	10	ABZ41635	ABZ41635 N. gonorr
25	17.4	75.7	402	10	ABZ41635	ABZ41635 N. gonorr
26	17.4	75.7	447	8	ACA14606	ACA14606 Prokaryot
27	17.4	75.7	448	8	ACA24956	ACA24956 Prokaryot
28	17.4	75.7	468	8	ACA49510	ACA49510 Prokaryot
29	17.4	75.7	476	5	AAH89338	AAH89338 DNA encod
30	17.4	75.7	567	10	ABZ41132	ABZ41132 N. gonorr
31	17.4	75.7	567	10	ABZ41132	ABZ41132 N. gonorr
32	17.4	75.7	609	13	ADR93608	ADR93608 Novel S.
33	17.4	75.7	693	13	ABX66003	ABX66003 Helicobac
34	17.4	75.7	785	4	AAH89144	AAH89144 Polyketid
35	17.4	75.7	882	2	AAV37148	AAV37148 DNA sequ
36	17.4	75.7	882	4	AAH01743	AAH01743 Bacteroid
37	17.4	75.7	885	2	AAV37147	AAV37147 DNA sequ
38	17.4	75.7	885	4	AAH01742	AAH01742 Bacillus
39	17.4	75.7	888	2	AAV37151	AAV37151 DNA sequ
40	17.4	75.7	888	4	AAH01746	AAH01746 Chlamydia
41	17.4	75.7	888	4	AAH01762	AAH01762 Burkholder
42	17.4	75.7	891	2	AAV37160	AAV37160 DNA sequ
43	17.4	75.7	891	2	AAV37156	AAV37156 DNA sequ
44	17.4	75.7	891	2	AAV37163	AAV37163 DNA sequ
45	17.4	75.7	891	2	AAV37153	AAV37153 DNA sequ
46	17.4	75.7	891	2	AAV37161	AAV37161 DNA sequ
47	17.4	75.7	891	2	AAV37154	AAV37154 DNA sequ
48	17.4	75.7	891	2	AAV37158	AAV37158 DNA sequ
49	17.4	75.7	891	2	AAV37159	AAV37159 DNA sequ
50	17.4	75.7	891	2	AAV37162	AAV37162 DNA sequ
51	17.4	75.7	891	4	AAH01750	AAH01750 Micrococc
52	17.4	75.7	891	4	AAH01754	AAH01754 Rickettsi
53	17.4	75.7	891	4	AAH01752	AAH01752 Mycoplasma
54	17.4	75.7	891	4	AAH01675	AAH01675 Escherich
55	17.4	75.7	891	4	AAH01753	AAH01753 Neisseria
56	17.4	75.7	891	4	AAH01751	AAH01751 Mycobacte
57	17.4	75.7	891	4	AAH00619	AAH00619 Haemophil
58	17.4	75.7	891	4	AAH01755	AAH01755 Salmonell
59	17.4	75.7	891	4	AAH01747	AAH01747 Fibrobact
60	17.4	75.7	894	2	AAV37155	AAV37155 DNA sequ
61	17.4	75.7	894	2	AAV37150	AAV37150 DNA sequ
62	17.4	75.7	894	2	AAV37166	AAV37166 DNA sequ
63	17.4	75.7	894	4	AAH01745	AAH01745 Brevibact
64	17.4	75.7	894	4	AAH01011	AAH01011 Streptococ
65	17.4	75.7	894	4	AAH01748	AAH01748 Flavobact
66	17.4	75.7	894	5	AAH89341	AAH89341 DNA encod
67	17.4	75.7	894	5	AAH89387	AAH89387 DNA encod
68	17.4	75.7	895	5	AAH81954	AAH81954 DNA encod
69	17.4	75.7	895	5	AAH81927	AAH81927 DNA encod
70	17.4	75.7	897	2	AAV37165	AAV37165 DNA sequ
71	17.4	75.7	897	2	AAV37167	AAV37167 DNA sequ
72	17.4	75.7	897	2	AAV37146	AAV37146 DNA sequ
73	17.4	75.7	897	4	AAH01757	AAH01757 Stigmata
74	17.4	75.7	897	4	AAH01741	AAH01741 Agrobacte
75	17.4	75.7	897	4	AAH01758	AAH01758 Thiomonas
76	17.4	75.7	900	4	AAH02145	AAH02145 Pseudomon
77	17.4	75.7	906	2	AAV37157	AAV37157 DNA sequ
78	17.4	75.7	906	4	AAH01749	AAH01749 Helicobac
79	17.4	75.7	909	2	AAV37170	AAV37170 DNA sequ
80	17.4	75.7	909	4	AAH01761	AAH01761 Molinella
81	17.4	75.7	918	8	ACA43747	ACA43747 Prokaryot
82	17.4	75.7	950	8	ACA35266	ACA35266 Prokaryot
83	17.4	75.7	968	2	AAV90742	AAV90742 Nucleotid
84	17.4	75.7	970	2	AAV90873	AAV90873 Nucleotid
85	17.4	75.7	1098	10	ABZ41217	ABZ41217 N. gonorr
86	17.4	75.7	1098	10	ABZ41687	ABZ41687 N. gonorr
87	17.4	75.7	1105	6	ABH83108	ABH83108 Schizosac
88	17.4	75.7	1122	10	ADH83376	ADH83376 Enterococ
89	17.4	75.7	1131	10	ADH83352	ADH83352 E. faeciu
90	17.4	75.7	1155	9	ADA30260	ADA30260 DNA encod
91	17.4	75.7	1170	2	AAO20217	AAO20217 Sequence
92	17.4	75.7	1182	4	AAH51937	AAH51937 Staphyloc
93	17.4	75.7	1182	8	ABT14914	ABT14914 Pathogen

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 22:08:52 ; Search time 874.442 Seconds  
(without alignments)  
1274.492 Million cell updates/sec

Title: US-10-089-177-697

Perfect score: 23  
Sequence: 1 cnaagcgnckncrcrcycrcg 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 239416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database :

Genembl:\*  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pac:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	75.7	23	6	AX109964 Sequence
2	17.4	75.7	23	6	BD023040 Sequence
3	17.4	75.7	135	6	CO649882 Sequence
4	17.4	75.7	189	6	AR348991 Sequence
5	17.4	75.7	330	6	AR346992 Sequence
6	17.4	75.7	485	1	SMU75481 Sequence
7	17.4	75.7	693	1	AX788739 Sequence
8	17.4	75.7	723	1	SPRPS10A Sequence
9	17.4	75.7	762	1	AF295388 Sequence
10	17.4	75.7	882	6	AX111003 Sequence
11	17.4	75.7	882	6	BD023081 Sequence
12	17.4	75.7	885	6	AX111002 Sequence
13	17.4	75.7	885	6	BD023080 Sequence
14	17.4	75.7	888	6	AX111006 Sequence
15	17.4	75.7	888	6	AX111022 Sequence
16	17.4	75.7	888	6	BD023084 Sequence
17	17.4	75.7	891	6	AX109877 Sequence
18	17.4	75.7	891	6	AX110935 Sequence
19	17.4	75.7	891	6	AX111007 Sequence

C 20	17.4	75.7	891	6	AX111010 Sequence
C 21	17.4	75.7	891	6	AX111011 Sequence
C 22	17.4	75.7	891	6	AX111012 Sequence
C 23	17.4	75.7	891	6	AX111013 Sequence
C 24	17.4	75.7	891	6	AX111014 Sequence
C 25	17.4	75.7	891	6	AX111015 Sequence
C 26	17.4	75.7	891	6	BD023086 Sequence
C 27	17.4	75.7	891	6	BD023087 Sequence
C 28	17.4	75.7	891	6	BD023089 Sequence
C 29	17.4	75.7	891	6	BD023091 Sequence
C 30	17.4	75.7	891	6	BD023092 Sequence
C 31	17.4	75.7	891	6	BD023093 Sequence
C 32	17.4	75.7	891	6	BD023094 Sequence
C 33	17.4	75.7	891	6	BD023095 Sequence
C 34	17.4	75.7	891	6	BD023096 Sequence
C 35	17.4	75.7	894	6	AX110269 Sequence
C 36	17.4	75.7	894	6	AX111005 Sequence
C 37	17.4	75.7	894	6	AX111008 Sequence
C 38	17.4	75.7	894	6	BD023083 Sequence
C 39	17.4	75.7	894	6	BD023088 Sequence
C 40	17.4	75.7	894	6	BD023099 Sequence
C 41	17.4	75.7	897	6	AX111017 Sequence
C 42	17.4	75.7	897	6	AX111018 Sequence
C 43	17.4	75.7	897	6	AX111019 Sequence
C 44	17.4	75.7	897	6	BD023079 Sequence
C 45	17.4	75.7	897	6	BD023098 Sequence
C 46	17.4	75.7	897	6	BD023100 Sequence
C 47	17.4	75.7	900	6	AX111405 Sequence
C 48	17.4	75.7	906	6	AX111009 Sequence
C 49	17.4	75.7	906	6	BD023090 Sequence
C 50	17.4	75.7	909	6	AX111021 Sequence
C 51	17.4	75.7	909	6	BD023103 Sequence
C 52	17.4	75.7	968	6	BD061867 Sequence
C 53	17.4	75.7	970	6	BD061998 Sequence
C 54	17.4	75.7	1043	2	PFMAL8PC1 Sequence
C 55	17.4	75.7	1122	1	AR395246 Sequence
C 56	17.4	75.7	1128	1	FGS85RTUF Sequence
C 57	17.4	75.7	1131	6	AR346368 Sequence
C 58	17.4	75.7	1140	1	SASGALTUF Sequence
C 59	17.4	75.7	1143	1	AF295387 Sequence
C 60	17.4	75.7	1149	1	CA636RTUF Sequence
C 61	17.4	75.7	1155	6	AR318997 Sequence
C 62	17.4	75.7	1176	1	AY099292 Sequence
C 63	17.4	75.7	1176	1	AY099294 Sequence
C 64	17.4	75.7	1176	1	AY099295 Sequence
C 65	17.4	75.7	1182	1	AX583738 Sequence
C 66	17.4	75.7	1182	6	AX620422 Sequence
C 67	17.4	75.7	1185	6	AR089426 Sequence
C 68	17.4	75.7	1185	6	BD268414 Sequence
C 69	17.4	75.7	1185	6	CO817257 Sequence
C 70	17.4	75.7	1185	6	CO817259 Sequence
C 71	17.4	75.7	1185	6	AR330091 Sequence
C 72	17.4	75.7	1185	6	AR493528 Sequence
C 73	17.4	75.7	1185	6	AX109965 Sequence
C 74	17.4	75.7	1185	6	AX111364 Sequence
C 75	17.4	75.7	1185	6	AX363591 Sequence
C 76	17.4	75.7	1185	12	AY305395 Sequence
C 77	17.4	75.7	1185	12	AY305396 Sequence
C 78	17.4	75.7	1185	12	AY305397 Sequence
C 79	17.4	75.7	1188	12	AY305399 Sequence
C 80	17.4	75.7	1188	1	AB035461 Sequence
C 81	17.4	75.7	1188	1	AB035462 Sequence
C 82	17.4	75.7	1188	1	AB035463 Sequence
C 83	17.4	75.7	1188	1	AB035464 Sequence
C 84	17.4	75.7	1188	1	AB035465 Sequence
C 85	17.4	75.7	1188	1	AB035466 Sequence
C 86	17.4	75.7	1188	1	TOUUF Sequence
C 87	17.4	75.7	1188	1	CTUUF Sequence
C 88	17.4	75.7	1188	1	FP13524 Sequence
C 89	17.4	75.7	1191	1	AB073986 Sequence
C 90	17.4	75.7	1191	1	TCHESTUUF Sequence
C 91	17.4	75.7	1191	6	AR346768 Sequence
C 92	17.4	75.7	1191	6	AX110130 Sequence

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 23:02:39 / Search time 448.942 Seconds  
(without alignments)  
384.253 Million cell updates/sec

Title: US-10-089-177-664

Perfect score: 29  
Sequence: 1 aaygatnacngngcngcncaratgga 29

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapept 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 311075104

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database :

Published Applications NA.\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
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9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
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14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
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17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US10F\_NEW\_PUB.seq.\*  
20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23.2	80.0	29	US-09-989-643-107	Sequence 107, App
2	23.2	80.0	18	US-10-753-169-107	Sequence 107, App
3	23.2	80.0	70	US-10-282-122A-1961	Sequence 1961, App
4	23.2	80.0	70	US-10-282-122A-2519	Sequence 2519, App
5	23.2	80.0	70	US-10-282-122A-2519	Sequence 2519, App
6	23.2	80.0	111	US-10-282-122A-2376	Sequence 2376, App
7	23.2	80.0	130	US-09-815-242-2973	Sequence 2973, App
8	23.2	80.0	130	US-10-282-122A-5535	Sequence 5535, App
9	23.2	80.0	163	US-09-815-242-261	Sequence 261, App
10	23.2	80.0	163	US-10-282-122A-2556	Sequence 2556, App
11	23.2	80.0	183	US-10-282-122A-2416	Sequence 2416, App

12	23.2	80.0	184	US-09-815-242-2185	Sequence 2185, App
13	23.2	80.0	184	US-10-282-122A-4758	Sequence 4758, App
14	23.2	80.0	185	US-10-282-122A-1866	Sequence 1866, App
15	23.2	80.0	185	US-10-282-122A-2139	Sequence 2139, App
16	23.2	80.0	187	US-09-815-242-194	Sequence 194, App
17	23.2	80.0	187	US-09-815-242-198	Sequence 198, App
18	23.2	80.0	187	US-10-282-122A-184	Sequence 184, App
19	23.2	80.0	187	US-10-282-122A-202	Sequence 202, App
20	23.2	80.0	193	US-10-282-122A-2553	Sequence 2553, App
21	23.2	80.0	196	US-10-282-122A-3396	Sequence 3396, App
22	23.2	80.0	202	US-09-815-242-176	Sequence 176, App
23	23.2	80.0	202	US-10-282-122A-164	Sequence 164, App
24	23.2	80.0	222	US-10-282-122A-1777	Sequence 1777, App
25	23.2	80.0	222	US-10-282-122A-2570	Sequence 2570, App
26	23.2	80.0	236	US-09-815-242-301	Sequence 301, App
27	23.2	80.0	236	US-10-282-122A-280	Sequence 280, App
28	23.2	80.0	269	US-09-815-242-242	Sequence 242, App
29	23.2	80.0	269	US-10-282-122A-229	Sequence 229, App
30	23.2	80.0	275	US-10-282-122A-1789	Sequence 1789, App
31	23.2	80.0	275	US-10-282-122A-1952	Sequence 1952, App
32	23.2	80.0	275	US-10-282-122A-2705	Sequence 2705, App
33	23.2	80.0	277	US-09-294-093B-405	Sequence 405, App
34	23.2	80.0	329	US-10-282-122A-2708	Sequence 2708, App
35	23.2	80.0	332	US-10-282-122A-2146	Sequence 2146, App
36	23.2	80.0	341	US-10-282-122A-2394	Sequence 2394, App
37	23.2	80.0	341	US-10-282-122A-1933	Sequence 1933, App
38	23.2	80.0	343	US-10-282-122A-2252	Sequence 2252, App
39	23.2	80.0	369	US-10-282-122A-2252	Sequence 2252, App
40	23.2	80.0	390	US-10-282-122A-2619	Sequence 2619, App
41	23.2	80.0	501	US-10-424-5599-79597	Sequence 79597, App
42	23.2	80.0	566	US-10-282-122A-19211	Sequence 19211, App
43	23.2	80.0	572	US-10-449-857A-24	Sequence 24, App
44	23.2	80.0	580	US-09-815-242-782	Sequence 782, App
45	23.2	80.0	580	US-10-282-122A-747	Sequence 747, App
46	23.2	80.0	617	US-10-021-323-5496	Sequence 5496, App
47	23.2	80.0	628	US-10-282-122A-11485	Sequence 11485, App
48	23.2	80.0	656	US-09-939-980-87	Sequence 87, App
49	23.2	80.0	705	US-10-282-122A-16207	Sequence 16207, App
50	23.2	80.0	705	US-10-424-5599-12845	Sequence 12845, App
51	23.2	80.0	748	US-10-437-963-56273	Sequence 56273, App
52	23.2	80.0	840	US-10-424-5599-105909	Sequence 105909, App
53	23.2	80.0	846	US-10-282-122A-21226	Sequence 21226, App
54	23.2	80.0	884	US-10-425-115-1132	Sequence 1132, App
55	23.2	80.0	888	US-09-989-643-150	Sequence 150, App
56	23.2	80.0	888	US-10-753-169-150	Sequence 150, App
57	23.2	80.0	891	US-09-989-643-153	Sequence 153, App
58	23.2	80.0	891	US-09-989-643-154	Sequence 154, App
59	23.2	80.0	891	US-09-989-643-157	Sequence 157, App
60	23.2	80.0	891	US-09-989-643-159	Sequence 159, App
61	23.2	80.0	891	US-09-989-643-160	Sequence 160, App
62	23.2	80.0	891	US-09-989-643-161	Sequence 161, App
63	23.2	80.0	891	US-09-989-643-162	Sequence 162, App
64	23.2	80.0	891	US-09-989-643-163	Sequence 163, App
65	23.2	80.0	891	US-09-989-643-164	Sequence 164, App
66	23.2	80.0	891	US-09-989-643-170	Sequence 170, App
67	23.2	80.0	891	US-10-753-169-153	Sequence 153, App
68	23.2	80.0	891	US-10-753-169-154	Sequence 154, App
69	23.2	80.0	891	US-10-753-169-157	Sequence 157, App
70	23.2	80.0	891	US-10-753-169-159	Sequence 159, App
71	23.2	80.0	891	US-10-753-169-160	Sequence 160, App
72	23.2	80.0	891	US-10-753-169-161	Sequence 161, App
73	23.2	80.0	891	US-10-753-169-162	Sequence 162, App
74	23.2	80.0	891	US-10-753-169-163	Sequence 163, App
75	23.2	80.0	891	US-10-753-169-164	Sequence 164, App
76	23.2	80.0	891	US-10-753-169-170	Sequence 170, App
77	23.2	80.0	894	US-09-989-643-151	Sequence 151, App
78	23.2	80.0	894	US-09-989-643-156	Sequence 156, App
79	23.2	80.0	894	US-09-989-643-167	Sequence 167, App
80	23.2	80.0	894	US-09-989-643-169	Sequence 169, App
81	23.2	80.0	894	US-10-753-169-151	Sequence 151, App
82	23.2	80.0	894	US-10-753-169-156	Sequence 156, App
83	23.2	80.0	894	US-10-753-169-167	Sequence 167, App
84	23.2	80.0	894	US-10-753-169-169	Sequence 169, App

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OM nucleic - nucleic search, using sw model

Run on: March 16, 2005, 01:07:34 ; Search time 109.865 Seconds  
(without alignments)  
431.911 Million cell updates/sec

Title: US-10-089-177-664

Perfect score: 29  
Sequence: 1 aayacatnagngcngcncarcatgca 29

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%

Listing first 500 summaries

Database :  
1: Issued Patents NA:\*  
2: /cgn2\_6/prodata/1/ina/5A COMB. seq.\*  
3: /cgn2\_6/prodata/1/ina/SB COMB. seq.\*  
4: /cgn2\_6/prodata/1/ina/6A COMB. seq.\*  
5: /cgn2\_6/prodata/1/ina/6B COMB. seq.\*  
6: /cgn2\_6/prodata/1/ina/PCUTS COMB. seq.\*  
7: /cgn2\_6/prodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	23.2	80.0	656 3	US-08-936-165A-87 Sequence 87, App1
2	23.2	80.0	690 4	US-09-543-681A-2724 Sequence 2724, App
3	23.2	80.0	864 4	US-09-107-433-1775 Sequence 1775, App
4	23.2	80.0	929 4	US-09-710-279-1311 Sequence 1311, App
5	23.2	80.0	1113 4	US-09-489-039A-4624 Sequence 4624, App
6	23.2	80.0	1122 4	US-09-134-000C-1261 Sequence 1261, App
7	23.2	80.0	1131 4	US-09-107-532A-979 Sequence 979, App
8	23.2	80.0	1155 4	US-09-328-352-1547 Sequence 1547, App
9	23.2	80.0	1185 2	US-08-743-637B-185 Sequence 185, App
10	23.2	80.0	1185 3	US-09-218-197-1 Sequence 1, App1
11	23.2	80.0	1185 4	US-09-492-709A-86 Sequence 86, App1
12	23.2	80.0	1191 4	US-09-107-532A-1379 Sequence 1379, App
13	23.2	80.0	1191 4	US-09-902-540-8380 Sequence 8380, App
14	23.2	80.0	1191 4	US-09-583-110-747 Sequence 747, App
15	23.2	80.0	1224 4	US-09-252-991A-4775 Sequence 4775, App
16	23.2	80.0	1230 4	US-09-252-991A-4767 Sequence 4767, App
17	23.2	80.0	1230 4	US-09-252-991A-4767 Sequence 4767, App
18	23.2	80.0	1230 4	US-09-252-991A-4767 Sequence 4767, App
19	23.2	80.0	1245 3	US-09-134-001C-2540 Sequence 2540, App
20	23.2	80.0	1254 4	US-09-489-039A-3648 Sequence 3648, App
21	23.2	80.0	1260 4	US-09-489-039A-3750 Sequence 3750, App
22	23.2	80.0	1356 4	US-09-252-991A-4740 Sequence 4740, App
23	23.2	80.0	2273 4	US-09-902-540-3798 Sequence 3798, App
24	23.2	80.0	2996 3	US-08-961-527-260 Sequence 260, App
25	23.2	80.0	2997 4	US-09-710-879-3723 Sequence 3723, App
26	23.2	80.0	3173 4	US-09-581-822-7 Sequence 7, App1
27	23.2	80.0	7035 4	US-09-902-540-878 Sequence 878, App

28	23.2	80.0	15598 4	US-08-956-171B-82 Sequence 82, App1
29	23.2	80.0	15598 4	US-08-781-986A-82 Sequence 82, App1
30	23.2	80.0	18551 4	US-09-902-540-1187 Sequence 1187, App
31	23.2	80.0	49617 4	US-09-596-002-28 Sequence 28, App1
32	23.2	80.0	580073 4	US-08-545-528B-1 Sequence 1, App1
33	23.2	80.0	640681 4	US-09-790-988-1 Sequence 1, App1
34	23.2	80.0	1230025 4	US-09-198-452A-1 Sequence 1, App1
35	23.2	80.0	1230230 4	US-09-438-185A-1 Sequence 1, App1
36	23.2	80.0	1830121 4	US-09-557-884-1 Sequence 1, App1
37	23.2	80.0	1830121 4	US-09-557-884-1 Sequence 1, App1
38	23.2	80.0	1830121 4	US-09-643-990A-1 Sequence 1, App1
39	23.2	80.0	1830121 4	US-09-643-990A-1 Sequence 1, App1
40	23.2	80.0	1830121 4	US-09-643-990A-1 Sequence 1, App1
41	23.2	80.0	4403765 3	US-09-103-840A-2 Sequence 2, App1
42	21.6	74.5	2592 3	US-09-221-017B-642 Sequence 1, App1
43	20	69.0	1230 3	US-09-140-466-1 Sequence 1, App1
44	18.4	63.4	601 4	US-09-949-016-204685 Sequence 204685, App
45	18.4	63.4	122626 4	US-09-949-016-17524 Sequence 17524, App
46	17.8	61.4	636 4	US-09-543-681A-1862 Sequence 1862, App
47	17.4	60.0	601 4	US-09-949-016-136634 Sequence 136634, App
48	17.4	60.0	699 4	US-09-540-236-1842 Sequence 1842, App
49	17.4	60.0	99629 4	US-09-596-002-37 Sequence 37, App1
50	17.4	60.0	123463 4	US-09-949-016-17078 Sequence 17078, App
51	17.4	60.0	162914 4	US-09-949-016-15578 Sequence 15578, App
52	17	58.6	282 4	US-09-313-294A-2082 Sequence 2082, App
53	16.8	57.9	1747 4	US-09-949-016-1948 Sequence 1948, App
54	16.8	57.9	138282 4	US-09-949-016-15307 Sequence 15307, App
55	16.8	57.9	1664976 4	US-08-916-421B-1 Sequence 1, App1
56	16.8	57.9	1664976 4	US-09-692-570-1 Sequence 1, App1
57	16.4	56.6	601 4	US-09-949-016-66118 Sequence 66118, App
58	16.4	56.6	106 4	US-09-902-540-2989 Sequence 2989, App
59	16.4	56.6	1521 1	US-08-726-136-20 Sequence 20, App1
60	16.4	56.6	1521 3	US-09-103-434-20 Sequence 20, App1
61	16.4	56.6	1521 3	US-09-103-434-20 Sequence 20, App1
62	16.4	56.6	13332 4	US-09-902-540-1047 Sequence 1047, App
63	16.4	56.6	13821 4	US-09-949-016-13458 Sequence 13458, App
64	16.4	56.6	151089 4	US-09-949-016-14348 Sequence 14348, App
65	16.4	56.6	212139 4	US-09-949-016-16665 Sequence 16665, App
66	16.4	56.6	524032 4	US-09-949-016-16628 Sequence 16628, App
67	16.4	56.6	524032 4	US-09-949-016-16628 Sequence 16628, App
68	16.4	56.6	524032 4	US-09-949-016-16630 Sequence 16630, App
69	16.4	56.6	524032 4	US-09-949-016-16630 Sequence 16630, App
70	16.4	56.6	529885 4	US-09-949-016-14340 Sequence 14340, App
71	16.4	56.6	529885 4	US-09-949-016-14341 Sequence 14341, App
72	16.4	56.6	529885 4	US-09-949-016-14341 Sequence 14341, App
73	16.4	56.6	529885 4	US-09-949-016-14341 Sequence 14341, App
74	16.4	56.6	529885 4	US-09-949-016-14343 Sequence 14343, App
75	16.4	56.6	529885 4	US-09-949-016-14343 Sequence 14343, App
76	16.4	56.6	529885 4	US-09-949-016-14345 Sequence 14345, App
77	16.4	56.6	529885 4	US-09-949-016-14345 Sequence 14345, App
78	16.4	56.6	4403765 3	US-09-949-016-14347 Sequence 14347, App
79	16.4	56.6	4411529 3	US-09-103-840A-2 Sequence 2, App1
80	16.2	55.9	1020 4	US-09-396-196G-119074 Sequence 119074, App
81	16.2	55.9	1125 4	US-09-328-352-2425 Sequence 2425, App
82	16.2	55.9	1125 4	US-09-489-039A-3129 Sequence 3129, App
83	16.2	55.9	1436 4	US-09-328-352-2304 Sequence 2304, App
84	16.2	55.9	25466 4	US-09-526-192A-15 Sequence 15, App1
85	16.2	55.9	984 4	US-09-822-871-3 Sequence 3, App1
86	16.2	55.9	984 4	US-09-934-901-1 Sequence 1, App1
87	16	55.2	984 4	US-09-934-901-1 Sequence 1, App1
88	16	55.2	984 4	US-10-321-210-1 Sequence 1, App1
89	16	55.2	984 4	US-10-321-210-1 Sequence 1, App1
90	16	55.2	174429 4	US-09-949-016-12610 Sequence 12610, App
91	16	55.2	174430 4	US-09-949-016-12610 Sequence 12610, App
92	15.8	54.5	162 4	US-09-513-999C-29032 Sequence 29032, App
93	15.8	54.5	329 3	US-09-060-756-573 Sequence 573, App
94	15.8	54.5	431 3	US-09-670-314-573 Sequence 573, App
95	15.8	54.5	431 3	US-09-670-314-573 Sequence 573, App
96	15.8	54.5	431 3	US-09-670-314-573 Sequence 573, App
97	15.8	54.5	546 3	US-09-385-982-466 Sequence 466, App
98	15.8	54.5	601 4	US-09-949-016-18205 Sequence 18205, App
99	15.8	54.5	601 4	US-09-949-016-185430 Sequence 85430, App
100	15.8	54.5	601 4	US-09-949-016-126433 Sequence 126433, App

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 22:27:13 / Search time 2915.62 Seconds  
(without alignments)  
378.604 Million cell updates/sec

Title: US-10-089-177-664

Perfect score: 29

Sequence: 1 aaygatnagngngcngncaratgga 29

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_est3: \*  
4: gb\_est4: \*  
5: gb\_est5: \*  
6: gb\_est6: \*  
7: gb\_est7: \*  
8: gb\_est8: \*  
9: gb\_est9: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23.2	80.0	114	6	CB261364
2	23.2	80.0	146	4	BI360467
3	23.2	80.0	160	4	BG84781
4	23.2	80.0	160	4	BG895149
5	23.2	80.0	162	4	BI537234
6	23.2	80.0	174	1	AV414173
7	23.2	80.0	175	4	BU162805
8	23.2	80.0	194	8	CC059143
9	23.2	80.0	219	2	AM063192
10	23.2	80.0	220	9	CL898923
11	23.2	80.0	233	7	CF644038
12	23.2	80.0	266	1	AV418215
13	23.2	80.0	276	2	AM694494
14	23.2	80.0	313	7	CL898923
15	23.2	80.0	328	9	CL898923
16	23.2	80.0	344	2	AM063346
17	23.2	80.0	347	7	CF858624
18	23.2	80.0	350	7	T43567
19	23.2	80.0	352	7	CV513029
20	23.2	80.0	354	7	CR476346
21	23.2	80.0	355	1	AI486103
22	23.2	80.0	355	7	CN932021
23	23.2	80.0	380	8	AZ050022
24	23.2	80.0	385	2	AM064077

25	23.2	80.0	397	1	AV551304
26	23.2	80.0	399	6	CB655390
27	23.2	80.0	400	7	T04276
28	23.2	80.0	402	1	AV518885
29	23.2	80.0	402	2	BE521145
30	23.2	80.0	418	1	AU289247
31	23.2	80.0	418	4	BG263014
32	23.2	80.0	422	8	BH749989
33	23.2	80.0	424	5	BO622855
34	23.2	80.0	428	4	BM402658
35	23.2	80.0	431	1	AV408359
36	23.2	80.0	435	2	AM040690
37	23.2	80.0	443	5	BU993125
38	23.2	80.0	446	1	AV422863
39	23.2	80.0	449	2	BE54313
40	23.2	80.0	450	8	AZ326080
41	23.2	80.0	451	2	AM907286
42	23.2	80.0	455	6	CA516269
43	23.2	80.0	456	7	M89271
44	23.2	80.0	456	8	BZ349218
45	23.2	80.0	466	1	AI483744
46	23.2	80.0	466	9	CL903283
47	23.2	80.0	467	1	AV940013
48	23.2	80.0	467	6	CD275318
49	23.2	80.0	467	7	CO052070
50	23.2	80.0	470	9	CL903282
51	23.2	80.0	471	1	AV422343
52	23.2	80.0	474	8	BZ402639
53	23.2	80.0	475	7	CN942360
54	23.2	80.0	475	8	BZ402631
55	23.2	80.0	478	4	BI704013
56	23.2	80.0	479	4	BI267993
57	23.2	80.0	480	7	CV042450
58	23.2	80.0	481	8	AZ049142
59	23.2	80.0	482	1	AI778328
60	23.2	80.0	485	2	BF639445
61	23.2	80.0	485	1	AU060781
62	23.2	80.0	488	6	CD275520
63	23.2	80.0	490	4	BU803085
64	23.2	80.0	491	1	AU197422
65	23.2	80.0	492	5	BQ488762
66	23.2	80.0	493	7	CN547132
67	23.2	80.0	495	2	BE458790
68	23.2	80.0	496	5	BE070882
69	23.2	80.0	497	6	CB279706
70	23.2	80.0	497	6	CD658495
71	23.2	80.0	498	7	CF606638
72	23.2	80.0	501	7	CO746459
73	23.2	80.0	502	4	BU803992
74	23.2	80.0	505	7	CR994878
75	23.2	80.0	508	6	CB331112
76	23.2	80.0	510	2	BE921734
77	23.2	80.0	511	4	BG465515
78	23.2	80.0	511	2	AM675933
79	23.2	80.0	512	4	BM323718
80	23.2	80.0	514	4	BU758011
81	23.2	80.0	515	1	AV940645
82	23.2	80.0	516	6	CA524936
83	23.2	80.0	516	6	CD272559
84	23.2	80.0	516	9	AG267461
85	23.2	80.0	517	5	BO791087
86	23.2	80.0	518	1	AL613000
87	23.2	80.0	518	1	AV442731
88	23.2	80.0	518	2	AM257991
89	23.2	80.0	518	2	BE494337
90	23.2	80.0	518	2	T433908P
91	23.2	80.0	519	5	BP039049
92	23.2	80.0	519	6	CA905535
93	23.2	80.0	522	1	AV917158
94	23.2	80.0	524	4	BM066124
95	23.2	80.0	525	4	BG904292
96	23.2	80.0	526	8	AZ302919
97	23.2	80.0	527	6	CB331196

AV551304	AV551304
CB655390	OSJNCE08M
T04276	323 Lambdabm
AV518885	AV518885
BE521145	MT1734STM
AU289247	AU289247
BG263014	WHE0939
BH749989	SAIK_0306
BO622855	CC_Conf19
BM402658	SLA007C01
AV408359	AV408359
AM040690	EST283554
BU993125	HD12K107
AV422863	AV422863
BE54313	EST355656
AZ326080	476_d1040
AM907286	EST343409
CA516269	KS09055F1
M89271	CEL20D1 Chr
BZ349218	hg88604.g
AI483744	EST249615
CL903283	ACAB272/A
AV940013	AV940013
CD275318	T143B0287
CO052070	MdFw20561
CL903282	ACAB272/A
AV422343	AV422343
BZ402639	OGAA236TM
CN942360	010920AVB
BZ402631	OGAA236TC
BI704013	kt65d06.y
BI267993	NE116D041
CV042450	ta156b07.
AZ049142	GSSBRu054
AI778328	EST259207
BF639445	NF013F081
AU060781	AU060781
CD275520	T143B0155
BU803085	BU803085
AU197422	AU197422
BQ488762	19-B8455-
CN547132	EST_15121
BE458790	EST414082
BE070882	BE070882
CB279706	tu85g06.y
CD658495	EESTeE34
CF606638	GEMMA01.0
CO746459	cah90f12.
BU803992	BU803992
CR994878	041C04R1.
CB331112	3529_1_33
BE921734	EST425503
BG465515	RH122_45
AM675933	EST6_10937
BM323718	PIC1_22_E
BU758011	BU758011
AV940645	AV940645
CA524936	KS1204581
CD272559	T143B0663
AG267461	Cyantiid108
BO791087	E3907_Chl
AL613000	AL613000
AV442731	AV442731
AM257991	687065D08
BE494337	WHE1253.D
T433908P	AI481727.T_bruce1
BP039049	BP039049
CA905535	PCSC16701
AV917158	AV917158
BM066124	KS07011A0
BG904292	Talr1131A
AZ302919	GSSBRu186
CB331196	3529_1_34



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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:46:58 ; Search time 373.654 Seconds  
(without alignments)  
459.443 Million cell updates/sec

Title: US-10-089-177-664

Perfect score: 29

Sequence: 1 aayagatnaacngngcngcncaratgga 29

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 500 summaries

Database : N\_Geneseq\_1dec04:\*

1: Geneseq1980s:\*\n2: Geneseq1990s:\*\n3: Geneseq2000s:\*\n4: Geneseq2001as:\*\n5: Geneseq2001bs:\*\n6: Geneseq2002as:\*\n7: Geneseq2002bs:\*\n8: Geneseq2003as:\*\n9: Geneseq2003bs:\*\n10: Geneseq2003cs:\*\n11: Geneseq2003ds:\*\n12: Geneseq2004as:\*\n13: Geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23.2	80.0	29	AAV37106	Aav37106 Oligonuc1
2	23.2	80.0	29	AAH00673	Aah00673 Universal
3	23.2	80.0	29	ACF05433	Act05433 Universal
4	23.2	80.0	70	ACA14649	Act14649 Prokaryot
5	23.2	80.0	70	ACA14091	Act14091 Prokaryot
6	23.2	80.0	70	ACA14857	Act14857 Prokaryot
7	23.2	80.0	111	ACA14506	Act14506 Prokaryot
8	23.2	80.0	130	AAS50396	Aas50396 Staphyloc
9	23.2	80.0	130	ACA17665	Act17665 Prokaryot
10	23.2	80.0	163	AAS47684	Aas47684 Enterococ
11	23.2	80.0	163	ACA12386	Act12386 Prokaryot
12	23.2	80.0	183	ACA14546	Act14546 Staphyloc
13	23.2	80.0	184	AAS49608	Aas49608 Staphyloc
14	23.2	80.0	184	ACA16888	Act16888 Prokaryot
15	23.2	80.0	185	ACA14269	Act14269 Prokaryot
16	23.2	80.0	185	ACA13966	Act13966 Prokaryot
17	23.2	80.0	187	AAS47621	Aas47621 Enterococ
18	23.2	80.0	187	AAS47617	Aas47617 Enterococ
19	23.2	80.0	187	ACA12332	Act12332 Prokaryot
20	23.2	80.0	187	ACA12314	Act12314 Prokaryot

C 21	23.2	80.0	193	8	ACA14683	Act14683 Prokaryot
C 22	23.2	80.0	196	4	ACA15526	Act15526 Prokaryot
C 23	23.2	80.0	202	4	AAS47599	Aas47599 Enterococ
C 24	23.2	80.0	202	8	ACA12394	Act12394 Prokaryot
C 25	23.2	80.0	222	8	ACA13907	Act13907 Prokaryot
C 26	23.2	80.0	222	8	ACA14700	Act14700 Prokaryot
C 27	23.2	80.0	236	4	AAS47724	Aas47724 Enterococ
C 28	23.2	80.0	236	4	ACA12410	Act12410 Prokaryot
C 29	23.2	80.0	269	4	AAS47665	Aas47665 Enterococ
C 30	23.2	80.0	269	8	ACA12359	Act12359 Prokaryot
C 31	23.2	80.0	275	8	ACA14082	Act14082 Prokaryot
C 32	23.2	80.0	275	8	ACA14835	Act14835 Prokaryot
C 33	23.2	80.0	275	8	ACA13919	Act13919 Prokaryot
C 34	23.2	80.0	277	6	ABL71031	AbL71031 Corn taas
C 35	23.2	80.0	329	8	ACA14838	Act14838 Prokaryot
C 36	23.2	80.0	332	8	ACA14276	Act14276 Prokaryot
C 37	23.2	80.0	341	8	ACA14524	Act14524 Prokaryot
C 38	23.2	80.0	341	8	ACA14657	Act14657 Prokaryot
C 39	23.2	80.0	343	8	ACA14063	Act14063 Prokaryot
C 40	23.2	80.0	369	8	ACA14382	Act14382 Prokaryot
C 41	23.2	80.0	385	2	AAX89749	Aax89749 Synthetic
C 42	23.2	80.0	390	8	ACA14749	Act14749 Prokaryot
C 43	23.2	80.0	467	9	ACL15425	Act15425 DNA clone
C 44	23.2	80.0	515	9	ACL15426	Act15426 DNA clone
C 45	23.2	80.0	532	9	ACL15433	Act15433 DNA clone
C 46	23.2	80.0	566	8	ACA31341	Act31341 Prokaryot
C 47	23.2	80.0	572	10	ADD28534	Add28534 Mouse cae
C 48	23.2	80.0	580	4	AAS48205	Aas48205 Enterococ
C 49	23.2	80.0	580	8	ACA12877	Act12877 Prokaryot
C 50	23.2	80.0	606	9	ACL15431	Act15431 DNA clone
C 51	23.2	80.0	608	9	ACL15428	Act15428 DNA clone
C 52	23.2	80.0	617	13	ACN50715	AcN50715 Cotton an
C 53	23.2	80.0	628	8	ACA23615	Act23615 Prokaryot
C 54	23.2	80.0	652	6	ABX66890	Abx66890 Helicobac
C 55	23.2	80.0	656	2	AAT83947	Aat83947 DNA encod
C 56	23.2	80.0	656	2	AAV53387	Aav53387 DNA encod
C 57	23.2	80.0	657	10	ABZ41637	Abz41637 N. gonorr
C 58	23.2	80.0	657	10	ABZ41137	Abz41137 N. gonorr
C 59	23.2	80.0	662	6	ABX66333	Abx66333 Helicobac
C 60	23.2	80.0	690	10	ADF02439	Adf02439 Bacteri
C 61	23.2	80.0	705	8	ACA28337	Act28337 Prokaryot
C 62	23.2	80.0	720	10	ABZ41639	Abz41639 N. gonorr
C 63	23.2	80.0	744	5	ABZ41141	Abz41141 N. gonorr
C 64	23.2	80.0	744	5	AAS81943	Aas81943 DNA encod
C 65	23.2	80.0	779	10	ACF66884	Act66884 Phototrab
C 66	23.2	80.0	846	8	ACA33356	Act33356 Prokaryot
C 67	23.2	80.0	864	13	ADR93140	Adr93140 Novel S.
C 68	23.2	80.0	888	4	AAH01744	Aah01744 DNA seque
C 69	23.2	80.0	888	4	AAH01744	Aah01744 Borrella
C 70	23.2	80.0	891	2	AAV37160	Aav37160 DNA seque
C 71	23.2	80.0	891	2	AAV37152	Aav37152 DNA seque
C 72	23.2	80.0	891	2	AAV37156	Aav37156 DNA seque
C 73	23.2	80.0	891	2	AAV37163	Aav37163 DNA seque
C 74	23.2	80.0	891	2	AAV37169	Aav37169 DNA seque
C 75	23.2	80.0	891	2	AAV37153	Aav37153 DNA seque
C 76	23.2	80.0	891	2	AAV37161	Aav37161 DNA seque
C 77	23.2	80.0	891	2	AAV37158	Aav37158 DNA seque
C 78	23.2	80.0	891	2	AAV37159	Aav37159 DNA seque
C 79	23.2	80.0	891	2	AAV37162	Aav37162 DNA seque
C 80	23.2	80.0	891	4	AAH01750	Aah01750 Micrococ
C 81	23.2	80.0	891	4	AAH01754	Aah01754 Rickettsi
C 82	23.2	80.0	891	4	AAH01752	Aah01752 Mycoplasma
C 83	23.2	80.0	891	4	AAH01675	Aah01675 Escherich
C 84	23.2	80.0	891	4	AAH01753	Aah01753 Neisseria
C 85	23.2	80.0	891	4	AAH01751	Aah01751 Mycobacte
C 86	23.2	80.0	891	4	AAH00619	Aah00619 Haemophil
C 87	23.2	80.0	891	4	AAH01755	Aah01755 Salmonell
C 88	23.2	80.0	891	4	AAH01760	Aah01760 Ureaplasma
C 89	23.2	80.0	894	2	AAV37155	Aav37155 DNA seque
C 90	23.2	80.0	894	2	AAV37150	Aav37150 DNA seque
C 91	23.2	80.0	894	2	AAV37168	Aav37168 DNA seque
C 92	23.2	80.0	894	2	AAV37166	Aav37166 DNA seque
C 93	23.2	80.0	894	4	AAH01759	Aah01759 Treponema

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 22:08:52 ; Search time 1102.56 Seconds  
(without alignments)  
1274.492 Million cell updates/sec

Title: US-10-089-177-664

Perfect score: 29

Sequence: 1 aayatgatnagngngngncaratagga 29

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_bhg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_ats: \*  
12: gb\_ey: \*  
13: gb\_un: \*  
14: gb\_vl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23.2	80.0	29	6	AX109931 Sequence
2	23.2	80.0	29	6	BD023039 Species-s
3	23.2	80.0	385	6	BD137176 Automonu
4	23.2	80.0	652	6	AX790513 Sequence
5	23.2	80.0	654	1	AB025429 Synchoco
6	23.2	80.0	654	1	AB025430 Synchoco
7	23.2	80.0	656	6	AR194438 Sequence
8	23.2	80.0	662	6	AX789399 Sequence
9	23.2	80.0	688	1	GVU09433 Sequence
10	23.2	80.0	690	6	AR377718 Gloeobacter
11	23.2	80.0	700	1	AY661424 Candidatu
12	23.2	80.0	700	1	AY685053 Candidatu
13	23.2	80.0	703	1	PMU09445 Prochloroth
14	23.2	80.0	703	8	PMU09442 Pandorina m
15	23.2	80.0	703	8	BP009424 Bryopsis pl
16	23.2	80.0	705	8	CCU09429 Costaria co
17	23.2	80.0	705	8	CSU09426 Chlorella s
18	23.2	80.0	705	8	DMU09431 Desbisia ma
19	23.2	80.0	705	8	SMU09447 Smitthora na

20	23.2	80.0	706	1	GSU09434	U09434 Gloeotheca
21	23.2	80.0	706	1	PEU09443	U09443 Phormidium
22	23.2	80.0	706	8	DEU09432	U09432 Diaparnalid
23	23.2	80.0	706	8	GLU09436	U09436 Gracilaria
24	23.2	80.0	706	8	GPU09435	U09435 Gonium pect
25	23.2	80.0	706	8	LSU09437	U09437 Laminaria s
26	23.2	80.0	706	8	MSU09438	U09438 Mantoniella
27	23.2	80.0	706	8	ODU09440	U09440 Ochromonas
28	23.2	80.0	706	8	OSU09441	U09441 Odontella s
29	23.2	80.0	706	8	PSU09449	U09449 Porphyridiu
30	23.2	80.0	706	8	VB009448	U09448 Vaucheria b
31	23.2	80.0	709	1	NSU09439	U09439 Nitzelia tra
32	23.2	80.0	732	1	AF217548	AF217548 Buchnera
33	23.2	80.0	732	1	AF217549	AF217549 Buchnera
34	23.2	80.0	732	1	AF217550	AF217550 Buchnera
35	23.2	80.0	732	1	AF217551	AF217551 Buchnera
36	23.2	80.0	732	1	AF217552	AF217552 Buchnera
37	23.2	80.0	747	8	CBE544127	AY544127 Coccolith
38	23.2	80.0	747	8	CBE544125	AY544125 Coccolith
39	23.2	80.0	747	8	CBE544126	AY544126 Coccolith
40	23.2	80.0	747	8	CBE544128	AY544128 Coccolith
41	23.2	80.0	747	8	HC0544124	AY544124 Helicosph
42	23.2	80.0	747	8	HC0544134	AY544134 Helicosph
43	23.2	80.0	747	8	HHY544133	AY544133 Helicosph
44	23.2	80.0	747	8	PC0544131	AY544131 Pleurochr
45	23.2	80.0	747	8	PDE544132	AY544132 Pleurochr
46	23.2	80.0	747	8	UF0544130	AY544130 Umbilicos
47	23.2	80.0	747	8	US1544129	AY303553 Candidatu
48	23.2	80.0	768	1	AY303553	AY303553 Candidatu
49	23.2	80.0	798	1	AY303555	AY303555 Candidatu
50	23.2	80.0	802	1	AB095495	AB095495 Aster yel
51	23.2	80.0	802	1	AB095667	AB095667 Aster yel
52	23.2	80.0	802	1	AB095668	AB095668 Aster yel
53	23.2	80.0	802	1	AB095669	AB095669 Aster yel
54	23.2	80.0	802	1	AB095670	AB095670 Aster yel
55	23.2	80.0	802	1	AB095671	AB095671 Aster yel
56	23.2	80.0	802	1	AB095672	AB095672 Paulownia
57	23.2	80.0	802	1	AB095673	AB095673 Tsunabuki
58	23.2	80.0	804	1	AB095674	AB095674 Western X
59	23.2	80.0	804	1	AY303556	AY303556 Candidatu
60	23.2	80.0	804	1	AY303571	AY303571 Candidatu
61	23.2	80.0	805	1	PSY18215	Y18215 Papaya dieb
62	23.2	80.0	812	1	AR465542	AR465542 Buchnera
63	23.2	80.0	858	8	AT391373	AY391373 Galdieria
64	23.2	80.0	862	1	AY303552	AY303552 Candidatu
65	23.2	80.0	862	1	AY303554	AY303554 Candidatu
66	23.2	80.0	867	8	AY454403	AY454403 Percusar
67	23.2	80.0	870	8	AY568054	AY568054 Pinus kor
68	23.2	80.0	875	8	AY454409	AY454409 Acrochaet
69	23.2	80.0	879	8	AY454417	AY454417 Halochlor
70	23.2	80.0	880	8	AY454418	AY454418 Bolebocole
71	23.2	80.0	881	8	AY454412	AY454412 Acrochaet
72	23.2	80.0	882	8	AY454415	AY454415 Phaeophill
73	23.2	80.0	882	8	AY568053	AY568053 Klebsorni
74	23.2	80.0	883	8	AY454419	AY454419 Bolebocole
75	23.2	80.0	884	8	AY454422	AY454422 Pseudoneo
76	23.2	80.0	885	8	AY454416	AY454416 Phaeophill
77	23.2	80.0	886	6	AY454424	AY454424 Uloclitrix
78	23.2	80.0	888	6	AX111004	AX111004 Sequence
79	23.2	80.0	888	6	BD023082	BD023082 Species-s
80	23.2	80.0	891	6	AX109877	AX109877 Sequence
81	23.2	80.0	891	6	AX110935	AX110935 Sequence
82	23.2	80.0	891	6	AX111010	AX111010 Sequence
83	23.2	80.0	891	6	AX111011	AX111011 Sequence
84	23.2	80.0	891	6	AX111012	AX111012 Sequence
85	23.2	80.0	891	6	AX111013	AX111013 Sequence
86	23.2	80.0	891	6	AX111014	AX111014 Sequence
87	23.2	80.0	891	6	AX111015	AX111015 Sequence
88	23.2	80.0	891	6	AX111020	AX111020 Sequence
89	23.2	80.0	891	6	BD023085	BD023085 Species-s
90	23.2	80.0	891	6	BD023086	BD023086 Species-s
91	23.2	80.0	891	6	BD023089	BD023089 Species-s
92	23.2	80.0	891	6	BD023091	BD023091 Species-s